



#6

-1-

SEQUENCE LISTING

A2

<110> Hanke, Paul D.

<120> Feedback-Resistant Pyruvate Carboxylase Gene from *Corynebacterium*

<130> 1533.1230001/MAC/RGM

<140> US 09/974,973

<141> 2001-10-12

<150> US 60/239,913

<151> 2000-10-13

Sub B15

<160> 19

<170> PatentIn version 3.0

<210> 1

<211> 3474

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

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Leu Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg	
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Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr	
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Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly	
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Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe	
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Leu Gly Asp Arg Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys	
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Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln	
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His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys	

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Asp	Leu	Pro	Val	His	Val	His	Thr	His	Asp	Thr	Ala	Gly	Gly	Gln	Leu	
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Ala Ala Lys	Lys 100	Val Lys Ala Asp 105	Ile Tyr Pro Gly Tyr 110	Gly Phe
Leu Ser Glu 115	Asn Ala Gln Leu 120	Ala Arg Glu Cys Ala 125	Glu Asn Gly Ile	
Thr Phe Ile Gly Pro Thr 130	Pro 135	Glu Val Leu Asp 140	Leu Thr Gly Asp Lys	
Ser Arg Ala Val Thr 145	Ala 150	Ala Lys Lys Ala 155	Gly Leu Pro Val Leu 160	Ala
Glu Ser Thr Pro 165	Ser 165	Lys Asn Ile Asp 170	Asp Ile Val Lys Ser 175	Ala Glu
Gly Gln Thr Tyr 180	Pro 180	Ile Phe Val Lys 185	Ala Val Ala Gly 190	Gly Gly Gly
Arg Gly Met Arg Phe Val Ser 195	Ser 200	Pro Asp Glu Leu Arg 205	Lys Leu Ala	
Thr Glu Ala Ser Arg Glu 210	Ala 215	Glu Ala Ala Phe 220	Gly Asp Gly Ser Val	
Tyr Val Glu Arg Ala Val 225	Ile 230	Asn Pro Gln His 235	Ile Glu Val Gln Ile 240	
Leu Gly Asp Arg Thr 245	Gly Glu Val Val 250	His Leu Tyr Glu Arg 255	Asp Cys	
Ser Leu Gln Arg 260	Arg His Gln Lys 265	Val Val Glu Ile Ala 270	Pro Ala Gln	
His Leu Asp Pro Glu Leu Arg 275	Asp 280	Arg Ile Cys Ala 285	Asp Ala Val Lys	
Phe Cys Arg Ser Ile Gly 290	Tyr 295	Gln Gly Ala Gly 300	Thr Val Glu Phe Leu	

Val Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile  
305 310 315 320

Gln Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val  
325 330 335

Lys Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly  
340 345 350

Leu Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg  
355 360 365

Ile Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr  
370 375 380

Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly  
385 390 395 400

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Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg  
420 425 430

Ala Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn  
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Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys  
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Val Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala  
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Pro Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly  
515 520 525

Ser Arg Asp Arg Leu Lys Gln Leu Gly Pro Ala Ala Phe Ala Arg Asp  
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Leu Arg Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp  
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Ala His Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys  
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Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val  
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Lys Ser Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu  
725 730 735

Arg Pro Ala Ala Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe  
740 745 750

Asp Leu Pro Val His Val His Thr His Asp Thr Ala Gly Gly Gln Leu  
755 760 765

Ala Thr Tyr Phe Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly  
770 775 780

Ala Ser Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala  
785 790 795 800

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Tyr Leu Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr 835 840 845		
Arg His Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala 850 855 860		
Thr Ala Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr 865 870 875 880		
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Ser Lys Val Val Gly Asp Leu Ala Leu His Leu Val Gly Ala Gly Val 900 905 910		
Asp Pro Ala Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp 915 920 925		
Ser Val Ile Ala Phe Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly 930 935 940		
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Lys Ala Pro Leu Thr Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp 965 970 975		
Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe 980 985 990		
Pro Lys Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn 995 1000 1005		
Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu 1010 1015 1020		
Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val Arg Thr Pro Leu 1025 1030 1035		
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<212> DNA

<213> Corynebacterium glutamicum

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cgtgaagatc ggggatcatt ccaccgctct tttgcttctg aagctgtccg cattggtact	240
gaaggctcac cagtcaaggc gtacctggac atcgatgaaa ttatcggtgc agctaaaaaa	300
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35 40 45

Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu  
50 55 60

Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala  
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Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu  
85 90 95

Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr  
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Ala	Ala	Glu	Ala	Val	Ala	Lys	Leu	Thr	Pro	Glu	Leu	Leu	Ser	Val	Glu	565	570	575
Ala	Trp	Gly	Gly	Ala	Thr	Tyr	Asp	Val	Ala	Met	Arg	Phe	Leu	Phe	Glu	580	585	590
Asp	Pro	Trp	Asp	Arg	Leu	Asp	Glu	Leu	Arg	Glu	Ala	Met	Pro	Asn	Val	595	600	605
Asn	Ile	Gln	Met	Leu	Leu	Arg	Gly	Arg	Asn	Thr	Val	Gly	Tyr	Thr	Pro	610	615	620
Tyr	Pro	Asp	Ser	Val	Cys	Arg	Ala	Phe	Val	Lys	Glu	Ala	Ala	Ser	Ser	625	630	635
Gly	Val	Asp	Ile	Phe	Arg	Ile	Phe	Asp	Ala	Leu	Asn	Asp	Val	Ser	Gln	645	650	655
Met	Arg	Pro	Ala	Ile	Asp	Ala	Val	Leu	Glu	Thr	Asn	Thr	Ala	Val	Ala	660	665	670
Glu	Val	Ala	Met	Ala	Tyr	Ser	Gly	Asp	Leu	Ser	Asp	Pro	Asn	Glu	Lys	675	680	685
Leu	Tyr	Thr	Leu	Asp	Tyr	Tyr	Leu	Lys	Met	Ala	Glu	Glu	Ile	Val	Lys	690	695	700
Ser	Gly	Ala	His	Ile	Leu	Ala	Ile	Lys	Asp	Met	Ala	Gly	Leu	Leu	Arg	705	710	715
Pro	Ala	Ala	Val	Thr	Lys	Leu	Val	Thr	Ala	Leu	Arg	Arg	Glu	Phe	Asp	725	730	735
Leu	Pro	Val	His	Val	His	Thr	His	Asp	Thr	Ala	Gly	Gly	Gln	Leu	Ala	740	745	750
Thr	Tyr	Phe	Ala	Ala	Ala	Gln	Ala	Gly	Ala	Asp	Ala	Val	Asp	Gly	Ala	755	760	765
Ser	Ala	Pro	Leu	Ser	Gly	Thr	Thr	Ser	Gln	Pro	Ser	Leu	Ser	Ala	Ile	770	775	780

Val	Ala	Ala	Phe	Ala	His	Thr	Arg	Arg	Asp	Thr	Gly	Leu	Ser	Leu	Glu	785	790	795	800
Ala	Val	Ser	Asp	Leu	Glu	Pro	Tyr	Trp	Glu	Ala	Val	Arg	Gly	Leu	Tyr	805	810	815	
Leu	Pro	Phe	Glu	Ser	Gly	Thr	Pro	Gly	Pro	Thr	Gly	Arg	Val	Tyr	Arg	820	825	830	
His	Glu	Ile	Pro	Gly	Gly	Gln	Leu	Ser	Asn	Leu	Arg	Ala	Gln	Ala	Thr	835	840	845	
Ala	Leu	Gly	Leu	Ala	Asp	Arg	Phe	Glu	Leu	Ile	Glu	Asp	Asn	Tyr	Ala	850	855	860	
Ala	Val	Asn	Glu	Met	Leu	Gly	Arg	Pro	Thr	Lys	Val	Thr	Pro	Ser	Ser	865	870	875	880
Lys	Val	Val	Gly	Asp	Leu	Ala	Leu	His	Leu	Val	Gly	Ala	Gly	Val	Asp	885	890	895	
Pro	Ala	Asp	Phe	Ala	Ala	Asp	Pro	Gln	Lys	Tyr	Asp	Ile	Pro	Asp	Ser	900	905	910	
Val	Ile	Ala	Phe	Leu	Arg	Gly	Glu	Leu	Gly	Asn	Pro	Pro	Gly	Gly	Trp	915	920	925	
Pro	Glu	Pro	Leu	Arg	Thr	Arg	Ala	Leu	Glu	Gly	Arg	Ser	Glu	Gly	Lys	930	935	940	
Ala	Pro	Leu	Thr	Glu	Val	Pro	Glu	Glu	Glu	Gln	Ala	His	Leu	Asp	Ala	945	950	955	960
Asp	Asp	Ser	Lys	Glu	Arg	Arg	Asn	Ser	Leu	Asn	Arg	Leu	Leu	Phe	Pro	965	970	975	
Lys	Pro	Thr	Glu	Glu	Phe	Leu	Glu	His	Arg	Arg	Arg	Phe	Gly	Asn	Thr	980	985	990	
Ser	Ala	Leu	Asp	Asp	Arg	Glu	Phe	Phe	Tyr	Gly	Leu	Val	Glu	Gly	Arg	995	1000	1005	
Glu	Thr	Leu	Ile	Arg	Leu	Pro	Asp	Val	Arg	Thr	Pro	Leu	Leu	Val		1010	1015	1020	
Arg	Leu	Asp	Ala	Ile	Ser	Glu	Pro	Asp	Asp	Lys	Gly	Met	Arg	Asn		1025	1030	1035	
Val	Val	Ala	Asn	Val	Asn	Gly	Gln	Ile	Arg	Pro	Met	Arg	Val	Arg		1040	1045	1050	
Asp	Arg	Ser	Val	Glu	Ser	Val	Thr	Ala	Thr	Ala	Glu	Lys	Ala	Asp		1055	1060	1065	
Ser	Ser	Asn	Lys	Gly	His	Val	Ala	Ala	Pro	Phe	Ala	Gly	Val	Val		1070	1075	1080	
Thr	Val	Thr	Val	Ala	Glu	Gly	Asp	Glu	Val	Lys	Ala	Gly	Asp	Ala		1085	1090	1095	
Val	Ala	Ile	Ile	Glu	Ala	Met	Lys	Met	Glu	Ala	Thr	Ile	Thr	Ala		1100	1105	1110	

A2  
cont.

Ser	Val	Asp	Gly	Lys	Ile	Asp	Arg	Val	Val	Val	Pro	Ala	Ala	Thr
1115						1120					1125			
Lys	Val	Glu	Gly	Gly	Asp	Leu	Ile	Val	Val	Val	Ser			
1130						1135					1140			

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